1. A method of identifying a therapeutic target, the method comprising the steps of:

(a) measuring protein or RNA levels of at least one component of an isolated mRNA ribonucleoprotein (mRNP) complex in a first sample enriched for a cell comprising a first phenotype; and

(b) comparing the levels determined in step (a) to the levels of the protein or RNA levels of the component in a second sample enriched for a cell comprising a second phenotype,

wherein if the levels of the component in the first sample are different from the levels of the component in the second sample, the component, a nucleic acid that encodes the component, or a protein encoded by the component is a potential therapeutic target for the treatment of a disease.

2. The method of claim 1, wherein the cell comprising the first phenotype is selected from the group consisting of a mature adipocyte, a preadipocyte, pancreatic beta cell, a hepatocyte, a skeletal muscle cell, and a cardiac muscle cell.

3. The method of claim 1, wherein the cell comprising the first phenotype is a mature adipocyte and the cell comprising the second phenotype is a preadipocyte.

4. The method of claim 1, wherein the first phenotype is a disease related to glucose or lipid metabolism and the second phenotype is a normal phenotype.

5. The method of claim 1, wherein the first phenotype is selected from the group consisting of obesity, diabetes, hypoglycemia, glucotoxicity, lipidtoxicity, insulin-resistance, hyperlipidemia, and lipodystrophy.

6. The method of claim 1, wherein the component is selected from the group consisting of an RNA binding protein, an RNA, and an mRNP-associated protein.

7. The method of claim 1, the method further comprising the step of:

(c) treating the sample in step (a) with an agent prior to measuring the protein or RNA levels of the component, wherein the agent alters the levels of at least one component of a glucose metabolic or a lipid metabolic pathway.

8. The method of claim 7, wherein the agent is selected from the group consisting of insulin, glucose, insulin-like growth factor-1 (IGF-1), a β-adrenergic agonist, glucose, glucagon-like peptide-1 (GLP-1), fatty acid, a peroxisome proliferator activated receptor (PPAR) ligand, and insulin-like growth factor 2 (IGF-2).

9. The method of claim 7, wherein the agent is a test therapeutic.

10. The method of claim 7, wherein the agent is selected from the group consisting of a nucleic acid, a protein, a peptide, or a small molecule.

11. The method of claim 1 or 7, further comprising the step of isolating the component, a nucleic acid encoding the component, or a protein encoded by the component.

12. The method of claim 1, wherein the component is Polypyrimidine Tract Binding Protein.

13. The method of claim 1, wherein the RNA binding protein is selected from the group consisting of the RNA binding proteins identified in Figure 10 to Figure 22.

14. The method of claim 1, wherein the component comprises a tag.

15. The method of claim 1, wherein the component is an mRNA that encodes a protein selected from the group consisting of a kinase, a transporter, a phosphatase, channel protein, a protease, a receptor, a transcription factor, and a transferase.

16. The method of claim 1, wherein the component is selected from the group consisting of 3-phosphoinositide dependent protein kinase-1, nuclear ubiquitous casein kinase 2, neural receptor protein-tyrosine kinase, MAP-kinase activating death domain, AMP-activated protein kinase beta-2 regulatory subunit, calcium/calmodulin-dependent protein kinase IV, Protein kinase C beta, adenylate kinase 3, mitogen activated protein kinase kinase 5, 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2, phosphatidylinositol 4-kinase, Glucokinase, glycogen synthase kinase 3 beta, phosphorylase kinase (gamma 2, testis), protein tyrosine phosphatase (non-receptor type 1), protein tyrosine phosphatase (non-receptor type 5), inositol polyphosphate-5-phosphatase D, Protein tyrosine phosphatase (receptor-type, zeta polypeptide), dual specificity phosphatase 6, protein tyrosine phosphatase (non-receptor type 12), glucose-6-phosphatase (catalytic), 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2, proton gated cation channel DRASIC, Sodium channel (nonvoltage-gated 1, alpha (epithelial)), calcium

channel (voltage-dependent, alpha2/delta subunit 1), Potassium inwardly-rectifying (channel, subfamily J, member 6), potassium channel regulator 1, calcium channel (voltage-dependent, T type, alpha 1G subunit), cyclic nucleotide-gated cation channel, amiloride-sensitive cation channel 1, potassium inwardly-rectifying channel J14, potassium large conductance calcium-activated channel (subfamily M, alpha member 1), potassium voltage gated channel (Shab-related subfamily, member 2), potassium channel subunit (Slack), potassium intermediate/small conductance calcium-activated channel (subfamily N, member 1), Sodium channel (voltage-gated, type V, alpha polypeptide), amiloride-sensitive cation channel 2 (neuronal), potassium channel (subfamily K, member 6 (TWIK-2)), cation-chloride cotransporter 6, solute carrier family 21 (organic anion transporter, member 12), amino acid transporter system A2, peptide/histidine transporter, choline transporter, solute carrier family 31 (copper transporters, member 1), solute carrier family 13 (sodium-dependent dicarboxylate transporter), solute carrier family 2 (facilitated glucose transporter, member 13), solute carrier family 12 (potassium-chloride transporter, member 5), Solute carrier family 6 (neurotransmitter transporter, serotonin, member 4), Solute carrier family 2 A2 (glucose transporter, type 2), carboxypeptidase D, ubiquitin specific protease 2, mast cell protease 1, proprotein convertase subtilisin / kexin, type 7, laminin receptor 1 (67kD, ribosomal protein SA), protein tyrosine phosphatase (non-receptor type 1), calcium-sensing receptor, neural receptor protein-tyrosine kinase, glutamate receptor (metabotropic 4), nuclear receptor subfamily 4 (group A, member 2), Neuropeptide Y5 receptor, protein tyrosine phosphatase (non-receptor type 5), insulin-like growth factor 1 receptor, Protein tyrosine phosphatase (receptor-type, zeta polypeptide), nuclear receptor subfamily 4 (group A, member 3), glutamate receptor (metabotropic 1), Tumor necrosis factor receptor superfamily (member 1a), insulin receptor, gamma-aminobutyric acid receptor associated protein, protein tyrosine phosphatase, non-receptor type 12, cholinergic receptor (nicotinic, beta polypeptide 1), olfactory receptor (U131), Gamma-aminobutyric acid receptor beta 2, glial cell line derived neurotrophic factor family receptor alpha 1, Glycine receptor beta, glutamate receptor interacting protein 2, adenylate cyclase activating polypeptide 1 receptor 1, asialoglycoprotein receptor 2, adenosine A3 receptor, Fibroblast growth factor receptor 1, nuclear receptor binding factor 2, purinergic receptor P2Y (G-protein coupled 1), nuclear receptor subfamily 1 (group H, member 4), peroxisome proliferator activator receptor(gamma), 5 hydroxytryptamine (serotonin) receptor 4, retinoid X receptor gamma, insulin receptor-related receptor, putative N-acetyltransferase Camello 4, lecithin-retinol acyltransferase, Phenylethanolamine N-methyltransferase, fucosyltransferase 2, Sialyltransferase 8 (GT3 alpha 2,8-sialyltransferase) C, UDP-

glucuronosyltransferase, alpha 1,3-fucosyltransferase Fuc-T (similar to mouse Fut4), diacylglycerol O-acyltransferase 1, signal transducer and activator of transcription 3, ISL1 transcription factor (LIM/homeodomain), and oligodendrocyte transcription factor 1.

17. The method of claim 16, wherein the protein is encoded by a gene selected from the group consisting of CNCG, CACNA2D1, KCNC3, and KCNB2.

18. A method for identifying a therapeutic target for the treatment of aberrant glucose metabolism or lipid metabolism, the method comprising the steps of:

(a) measuring RNA or protein levels of at least one component of an isolated mRNP complex in a first cell sample; and

(b) comparing RNA or protein levels determined in step (a) to the RNA or protein levels of the component from a second cell sample,

wherein if the levels of the component in the first sample are different from the levels of the component in the second sample, the component, a nucleic acid that encodes the component, or a protein encoded by the component is a potential therapeutic target for the treatment of the disease.

19. The method of claim 18, wherein the first cell sample is from an individual at risk of having a disease or who has a disease and the second cell sample is from a normal or healthy individual.

20. A method for identifying a therapeutic target related to the treatment of a disease, the method comprising the steps of:

(a) measuring RNA or protein levels of at least one component of an isolated mRNP complex in a sample that has been treated with an agent that alters the expression of a component of a glucose metabolic or lipid metabolic pathway; and

(b) comparing RNA or protein levels determined in step (a) to the RNA or protein levels of the component in an untreated control sample,

wherein if the levels of the component in the first sample are different from the levels of the component in the second sample, the component, a nucleic acid that encodes the component, or a

protein encoded by the component is a potential therapeutic target for the treatment of the disease.

21. A method for identifying a gene or gene product involved in a physiological pathway in a cell, the method comprising the steps of:

a. isolating an mRNP complex comprising at least one component that participates in a physiological pathway;

b. identifying at least one additional component of the isolated mRNP complex, wherein the additional component is also involved in a physiologicalpathway.

22. The method of claim 21, wherein the physiological pathway comprises a metabolic pathway or a regulatory pathway.

23. The method of claim 21, further comprising the step of confirming the activity of the additional component by inhibiting the expression of the additional component in a cell and determining the effect of the inhibition on metabolism.

24. The method of claim 23, wherein the inhibition step comprises inhibiting gene expression of the additional component using an agent selected from the group consisting of an RNAi, an antisense RNA, a ribozyme, and a PNA.

25. A method for identifying an agent that alters a physiological pathway, the method comprising the steps of:

a. subjecting a cell sample to an agent;

b. isolating an mRNP complex comprising at least one component that participates in a physiological pathway from the sample;

c. measuring the RNA or protein levels of at least one component of the isolated mRNP complex,

d. comparing the RNA or protein levels of step (c) to the RNA or protein levels of the component isolated from an untreated control sample,

wherein differential expression of the component in the agent-treated sample compared to the untreated control sample is indicative that the agent regulates the physiological pathway.

26. The method of claim 25, wherein the agent interacts with or regulates a component of the physiological pathway.

27. The method of claim 25, wherein the agent inhibits a physiologicalpathway.

28. The method of claim 25, wherein the agent enhances a physiologicalpathway.

29. The method of claim 25, wherein the physiological pathway is an insulin production pathway or a lipogenesis pathway.

30. A method for identifying a protein that regulates glucose metabolism, the method comprising the steps of:

a. measuring the expression in an isolated mRNP complex of at least one gene product of a cell involved in glucose metabolism, wherein the gene product is selected from the group consisting of an RNA binding protein, an mRNA associated with said RNA binding protein, or an mRNP complex-associated protein;

b. treating the cell with an agent selected from the group consisting of insulin, glucose, insulin-like growth factor-1 (IGF-1), a β-adrenergic agonist, glucose, glucagon-like peptide-1 (GLP-1), fatty acid, a peroxisome proliferator activated receptor (PPAR) ligand, and insulin-like growth factor 2 (IGF-2); and

c. measuring the expression of the gene product after treatment, wherein a difference in expression of the gene product after treatment compared to expression of the gene product before treatment is indicative that the protein regulates glucose metabolism.

31. A method for identifying an agent that regulates insulin production, the method comprising the steps of:

a. contacting a cell involves in insulin production with a nucleic acid capable of binding to at least one protein, wherein the protein is capable of binding to a 3' untranslated region or a 5' untranslated region of a preproinsulin mRNA;

b. separating the nucleic acid from the protein; and

c. identifying the protein.

32. The method of claim 31, wherein the protein binds to a nucleic acid comprising a sequence selected from the group consisting of 5'-gaauaaaaccuuugaaagagcacuac-3', 5'-cccaccacuacccuguccaccccucugcaaug-3', and 5'-agccctaagtgaccagctacagtcggaaaccatcagcaagcaggtcattgttccaac-3'.

33. An mRNP complex-associated with at least one of glucose or lipid metabolism, wherein the mRNP complex comprises a polypyrimidine tract binding (PTB) protein, and at least one mRNA associated with the polypyrimidine tract binding protein.

34. A method for identifying a component of an mRNP complex, the method comprising the steps of:

(a) transfecting a cell sample with a nucleic acid that inhibits the expression of an RNA binding protein;

(b) isolating total RNA from the cell sample and from a control sample;

(c) identifying RNAs that have altered expression in the nucleic acid-transfected sample compared to the control sample.

35. The method of any one of claims 1, 7, 18, and 20, wherein the disease is related to aberrant glucose or lipid metabolism.

36. The method of claim 21 or 25, wherein the physiological pathway comprises a glucose or lipid metabolic pathway.

37. The method of any one of claims 1, 17, 20, 25, and 30, wherein at least one of said measuring and said comparing steps comprises the use of an array.